

Title: *Nosema ceranae* Poses a New Threat to the European Honey Bees, *Apis mellifera*

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Abstract:

Globalization has provided opportunities for parasites/pathogens to cross geographic boundaries and expand to new hosts. Recent studies showed that *Nosema ceranae*, originally considered a microsporidian parasite of Eastern honey bees, *Apis cerana*, is, along with the long known resident species, *N. apis*, a disease agent in European honey bees, *A. mellifera*. In order to gain more insight into the epidemiology, pathogenicity, and evolution of *Nosema* parasitism in honey bees, we have used a genomic approach to determine 1) the presence, distribution, and historical occurrence of two *Nosema* species in both European and Asian honey bee hosts, 2) the tissue tropism, secondary structures of ribosomal RNA, and phylogenetic relationship of two *Nosema* species, 3) the complete sequences of the *N. ceranae* genome and nearly completed sequences of *N. apis* genome by 454 pyrosequencing technology. Our results showed that both *Nosema* species produced single and mixed infections in both European and Asian honey bees and that *N. ceranae* is much more invasive and predominant in the body of both species of honey bees than *N. apis*. While ultrastructural features showed that both species possess all of the characteristics of the genus *Nosema*, the tissue tropism was species specific which may lead to the difference of two *Nosema* species in host pathogenicity. Pyrosequence data of *N. ceranae* lead to a draft assembly (7.86 MB) and annotated genome, showing that the genome was highly AT-biased. Of 2,614 predicted protein-coding sequences, the genes conserved among microsporidia lack clear homology outside this group. Future comparisons of the genes conserved among microsporidia in two *Nosema* species will provide valuable insights and tools for identifying virulence factors in this group of the parasites. The genomic information will enable the researchers to pinpoint the signals that control gene function, which in turn should translate into new strategies for controlling and diminishing the effects of parasites and improving honey bee health.